Safe Drinking Water Partnerships: Microbiology at the Technical Support Center

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BACKGROUND

- The Office of Ground Water and Drinking Water (OGWDW) is responsible for developing and directing national policy for safeguarding national drinking water supplies from microbial and chemical contaminants.
 The Technical Support Center (TSC) of the OGWDW provides support to regulation development, regulation
- implementation, and analytical methods development and evaluation.
- > These objectives are achieved by frequent collaborations between several U.S. Environmental Protection Agency (U.S. EPA) offices, water utilities, and academic institutions.
- > Presented here are some of the collaborative efforts by the microbiology group of TSC.

ENTERIC VIRUSES

Introduction:

- > Enteric viruses have caused several waterborne outbreaks.
- ➤ Current detection methods for waterborne enteric viruses cannot differentiate between infectious and non-infectious states in all viruses.
- > An important public health issue is whether enteric viruses present in water samples are infectious.
- ➤ Goal of this project was to develop a rapid molecular method that differentiates between infectious and non-infectious viruses.

Method:

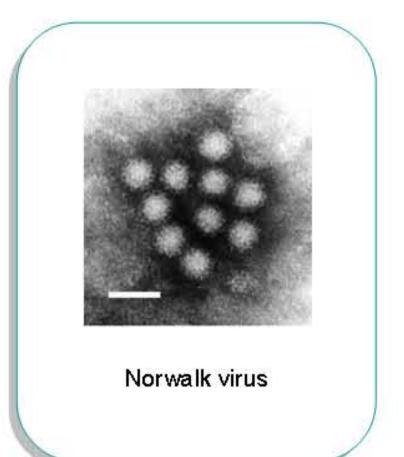
- ➤ Enteric viruses such as poliovirus, coxsackie virus, echovirus and Norwalk virus were inactivated by heat or chlorine.
- ➤ Inactivated and non-inactivated viruses were pretreated with Pronase E and RNase prior to Reverse Transcriptase Polymerase Chain Reaction (RT-PCR).
- ➤ Virus nucleic acid was extracted.
- > RT-PCR was performed and products were visualized on ethidium bromide stained gels.

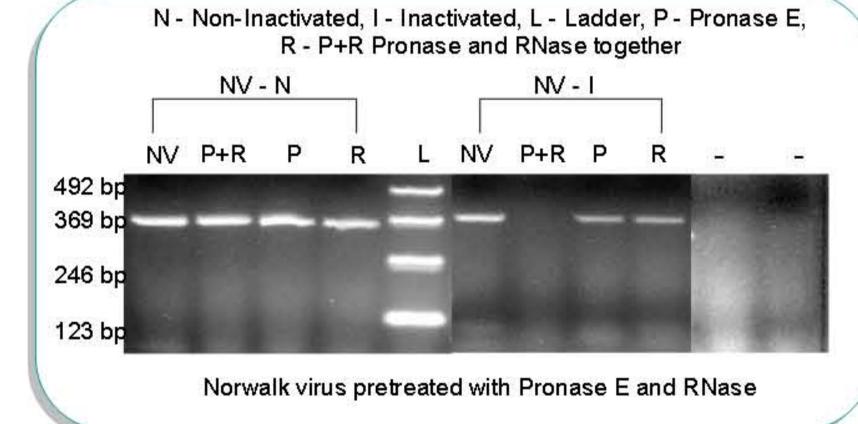
Results and Conclusions:

➤ Inactivated viruses yielded negative RT-PCR results while non-inactivated viruses yielded positive RT-PCR results when treated with Pronase E and RNase prior to RT-PCR.

INACTIVATED VIRUS INFECTIOUS VIRUS *W 00 00 Capsid intact Damaged Capsid Proteinase K Proteinase K **RNase RNase** 90 RNA Degraded RT-PCR **RNA** intact RT-PCR Negative results Positive results

Schematic representation of Pronase E and RNase pretreatment assay





CRYPTOSPORIDIUM MONITORING

CRYPTOSPORIDIUM MONITORING: Long Term 2 Enhanced Surface Water Treatment Rule (LT2) Proposed in 2004 Applicable to 7,000 public water systems (PWS) serving 180 million people PWS to conduct source water Cryptosporidium monitoring in the influent to drinking water plants that treat surface water or groundwater under the direct influence of surface water Monitoring results would indicate if additional Cryptosporidium treatment would be required In support of LT2, TSC Coordinates a Collaborates with Encourages proactive Cryptosporidium laboratory Cryptosporidium stakeholders nationwide for enhancing analytical methods monitoring approval program

AEROMONADS

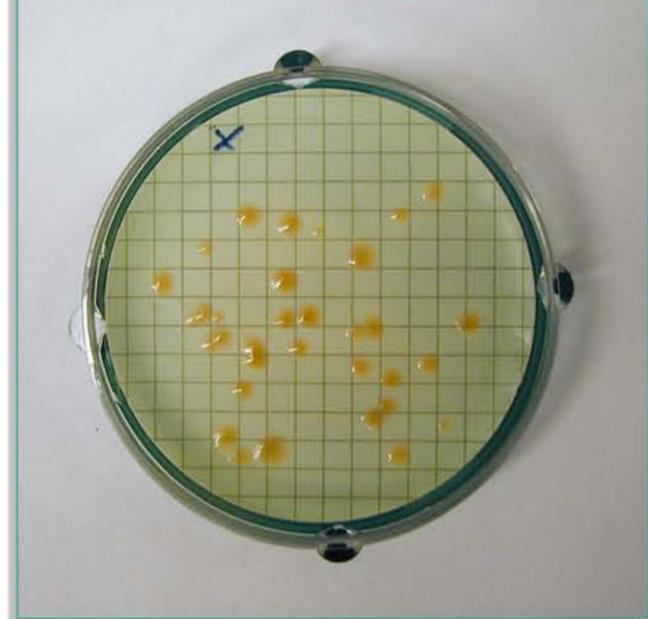
A. Small and Large scale monitoring of *Aeromonas*

Introduction:

- ➤ Aeromonas are autochthonous inhabitants of aquatic environments worldwide.
- ➤ Aeromonas are implicated as etiological agents in a variety of human diseases including gastroenteritis, wound infections, and septicemia.
- ➤ Goal of the project was to monitor for the presence of *Aeromonas* and to identify the different biotypes.

Methods:

- ➤ In a preliminary study, TSC collaborated with National Exposure Research Laboratory (ORD/NERL) to isolate and identify *Aeromonas* species from a small sample of drinking water distribution system supplies across the U.S.
- ➤ Aeromonas were also monitored for under the Unregulated Contaminant Monitoring Rule (UCMR) in 2003.
- ➤ 212 isolates that were obtained in the preliminary study were subjected to biochemical testing along with a Restriction Fragment Length Polymorphism (RFLP) analysis to type and identify the isolates to determine species.



Colonies of Aeromonas Hydrophila on ADA-V agar Plate

Results and Conclusions:

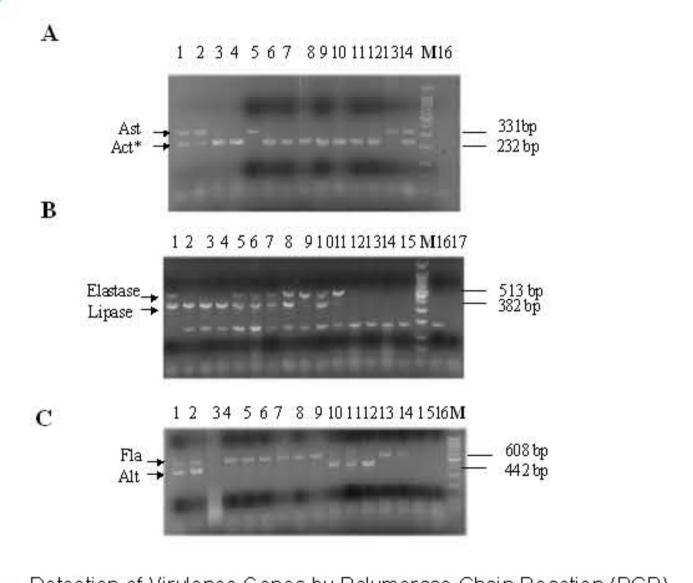
- > Several different biotypes of aeromonads were identified, including those that are suspected to be pathogenic to humans.
- > Aeromonas species isolated from the UCMR study are being further characterized by strain identification.

B. Virulence Factors of *Aeromonas* Introduction:

- The virulence of *Aeromonas* bacteria in causing diarrhea and other infections is generally believed to be multifactorial.
- An important concern to the EPA is whether *Aeromonas* species isolated from drinking water are potentially virulent.
- ➤ Goal of the project was to establish a method to characterize the virulence of *Aeromonas* isolates.

Methods:

- ➤ A genetic characterization of 8 virulence factor genes was performed using Polymerase Chain Reaction (PCR), with 52 drinking water isolates.
- ➤ Oligonucleotide primers to the genes, elastase (ahyB), lipase (pla), polar flagella (flaA/flaB, flaG), the enterotoxins alt, act and ast, and lateral flagella (lafA) were used in 4 duplex PCR assays.
- ➤ ORD/NERL performed animal model studies with immuno-compromised mice which were intraperitoneally injected with selected *Aeromonas* isolates.



Detection of Virulence Genes by Polymerase Chain Reaction (PCR)

Results and Conclusions:

- The genes ahyB, pla, flaA/B, flaG, act, alt and ast, and lafA were present in 88 %, 88%, 67 %, 68%, 69 %, 46%, 32% and 44% of the isolates, respectively.
- > Multiple species were isolated from most of the utilities and different combinations of virulence factors were observed in different strains of the same species.
- ➤ Isolates that had *lafA* or the lateral flagella gene, and one or more of the enterotoxin genes, showed clear signs of being virulent in animal studies.
- > 90 % of A hydrophila, 84 % of A. veronii, 100 % of A. caviae strains showed this correlation.
- > The other strains were avirulent as expected because they are not normally pathogenic to humans.

ALGAL TOXINS

